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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2003, 13:30:07 ; Search time 30.1827 Seconds
(without alignments)
2457.601 Million cell updates/sec

Title: US-09-807-933B-5
Perfect score: 1956
Sequence: 1 MKRLTIASSAIALAVGTEM.....TYKQVTCPIKATKSGCSRK 360

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPRMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteria:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match length	ID	Description
1	740	37.8	219	14	Q9JH92
2	735	37.6	219	14	Q9JH87
3	735	37.6	220	14	Q9JH84
4	734	37.5	220	14	Q9JH83
5	733	37.5	219	14	Q9JH91
6	730	37.3	217	14	Q9JH95
7	727	37.2	219	14	Q9JH90
8	727	37.2	219	14	Q9JH89
9	724	37.0	219	14	Q9JH88
10	721	36.9	221	14	Q9JH94
11	715	36.6	220	14	Q9JH93
12	714.5	36.5	218	14	Q9JH85
13	712	36.4	220	14	Q9JH96
14	711	36.3	219	14	Q9JH86
15	683.5	34.9	305	3	Q9J782
16	661.5	33.8	410	3	Q9P868

17	627.5	32.1	227	3	Q9J783	Q9J783 humicola gr
18	557.5	28.5	242	5	Q9J7401	Q9J7401 phaedon coc
19	555.5	28.4	271	3	Q9JVP3	Q9JVP3 alternaria
20	336	17.2	112	14	Q9JHA0	Q9JHA0 unclassified
21	331	16.9	112	14	Q9JH98	Q9JH98 unclassified
22	328	16.8	112	14	Q9JH99	Q9JH99 unclassified
23	320	16.4	112	14	Q9JHA1	Q9JHA1 unclassified
24	319	16.3	112	14	Q9JHA2	Q9JHA2 unclassified
25	312.5	16.0	111	14	Q9JH97	Q9JH97 unclassified
26	225	11.6	471	3	Q9HEV8	Q9HEV8 cricoderma
27	217	11.1	157	3	Q9P7F1	Q9P7F1 echizosach
28	204	10.4	476	3	Q9C1S9	Q9C1S9 humicola in
29	200	10.2	345	3	Q8W217	Q8W217 penicillium
30	188.5	9.6	439	3	Q9P893	Q9P893 agaricus bi
31	187.5	9.6	493	3	Q9P8D0	Q9P8D0 trichoderma
32	184.5	9.4	439	3	Q92401	Q92401 agaricus bi
33	179.5	9.2	888	5	Q25336	Q25336 leishmania
34	177.5	9.1	984	5	Q9Y1P7	Q9Y1P7 cryptospori
35	175.5	9.0	626	5	Q9NDD1	Q9NDD1 leishmania
36	174.5	8.9	629	5	Q9N745	Q9N745 leishmania
37	173.5	8.9	956	5	000908	000908 cryptospori
38	173	8.8	328	3	Q12140	Q12140 saccharomyc
39	173	8.8	648	5	Q9GY33	Q9GY33 leishmania
40	173	8.8	1217	5	Q17240	Q17240 bombyx mori
41	172	8.8	457	3	Q93837	Q93837 acromonium
42	171	8.7	351	2	Q9L8W0	Q9L8W0 mycoplasma
43	168.5	8.6	371	5	Q25333	Q25333 leishmania
44	168	8.6	576	2	Q9KJ33	Q9KJ33 enterococcu
45	168	8.6	1349	4	Q8WMO4	Q8WMO4 homo sapien

ALIGNMENTS

RESULT 1

Q9JH92 ID Q9JH92 PRELIMINARY; PRT; 219 AA.
AC Q9JH92;
DT 01-OCT-2000 (TREMBL:rel. 15, Created)
DT 01-OCT-2000 (TREMBL:rel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBL:rel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohnoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045171; BAA98041.1; -
DR HSSP; P43316; ZENG.
DR InterPro; IPR00334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_P45; UNKNOWN 1.
SQ SEQUENCE 219 AA; 23001 MW; 5F2EB81A6DBE26CE CRC64;.

Qy	Query Match	37.8%; Score 740; DB 14; Length 219;
Qy	Best Local Similarity	64.7%; Pred. No. 4.7e-39;
Db	Matches 134; Conservative 22; Mismatches 45; Indels 6; Gaps 4;	
Qy	155 NGETRRYWDCKSPSCWPKGADVTSPVGSCKNKOCT-LADNNT-QNCVGSSTYTCNDNO 212	
Db	16 SGRTRRYWDCKSKACAEKKAAYTPVDTCCKDSTTVASVDTVKSCDGGEGTMCYDQA 75	
Qy	213 PMVSDLAAYGAFAASISGSEATWCCAFELFTSTAVKGRVVVTVNTGSLGNTG 272	
Db	76 PMAVNDSVAAYGFAAACCAG-ESGACCCNCELTSTSPVNGKRVVQVTNTGSLGNS-- 132	
Qy	273 AHFDLQMPGGGVGTYNCATQWGAPTDGGARVGVSSASDSCNLPALQAGCKWRGWF 332	
Db	133 -QFLAIPGGGVGTYNCCTQOOSGAPADGMSRYGVSSRBCSQLPGLQAGCQWRDWF 191	

QY 333 KNADNPTMYKYVTCPEKAITAKSGCSR 359
 Db 192 QNADNPSINFNVQTCPELTAIKNCR 218

RESULT 2

Q9JH87 PRELIMINARY; PRT; 219 AA.
 AC Q9JH87; 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 OX NCBI_TaxID=42452;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
 RT "Diverse genes of family 45 cellulase homologues of the symbiotic
 RT protists in the hindgut of termite Reticulitermes speratus.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB045176; BAA98046.1; -
 DR HSSP: P43316; 2ENG.
 DR InterPro: IPR000334; GH_45.
 DR Pfam: PF02015; Glyco_hydro_45; 1.
 DR PROSITE: PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
 SQ SEQUENCE 219 AA; 23134 MW; 4BDEF4EC9ACC772D CRC64;

Query Match

Best Local Similarity 37.6%; Score 735; DB 14; Length 219;
 Best Local Similarity 61.7%; Pred. No. 9.6e-39;
 Matches 132; Conservative 28; Mismatches 48; Indels 6; Gaps 4;

QY 148 VSGAGSGEETRYWDCCKPSCSWPGKADVTSPVSGCNKDGT-LADNNT-QNGCVGSS 205
 Db 9 ISMSLADSGRTTRTYWDCCKSGCMEKKANVDKPIIDICADGTRVASNDTVSGCDGDDG 68
 QY 206 YTCNDNPNWYVSDLAIFPAASISGSEATWCCACFELFTSTAVKGMVQVNTGSD 265
 Db 69 FMCYDQTPWVSDLSLGFPAACCGG-ESGACCGCYELFTSGPVGKMMVQVNTGSD 127
 QY 266 DLGSNTGAHFDLQMPGGGVIYNGCATOWGAPTDGARGVSSASDCSNLPSALQAGC 325
 Db 128 DLGSN---QFDLAIPEGGVIGYNGCTAQSGAPSDGMSRGVSSRSRSCQSLPSGLQAGC 184
 QY 326 KMRFGMRNADNPTMYKYVTCPEKAITAKSGCSR 359
 Db 185 QMRFDWQONADNPSINFNVQTCPELTAIKNCR 218

RESULT 3

Q9JH84 PRELIMINARY; PRT; 220 AA.
 AC Q9JH84; 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 OX NCBI_TaxID=42452;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
 RT "Diverse genes of family 45 cellulase homologues of the symbiotic
 RT protists in the hindgut of termite Reticulitermes speratus.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB045179; BAA98049.1; -
 DR HSSP: P43316; 2ENG.
 DR InterPro: IPR000334; GH_45.
 DR Pfam: PF02015; Glyco_hydro_45; 1.
 DR PROSITE: PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.

SQ SEQUENCE 220 AA; 23274 MW; 26AF5357512EA061 CRC64;

Query Match 37.6%; Score 735; DB 14; Length 220;
 Best Local Similarity 64.3%; Pred. No. 9.6e-39;
 Matches 133; Conservative 21; Mismatches 47; Indels 6; Gaps 4;

QY 155 NGETTRYWDCCKPSCSWPGKADVTSPVSGCNKDGT-LADNNT-QNGCVGSSITCNDQ 212
 Db 17 SGKTRTRYWDCCKSGCMEKKAAVTPDTCGDGTRLASNDTVSSCDGDDGYMCYDQ 76
 QY 213 PMVVSDDLAVGFAAASISGSEATWCCACFELFTSTAVKGMVQVNTGSDLSNTG 272
 Db 77 PMAVNDSVAIFPAACCGG-ETGACCCYELFTSGPVGKMMVQVNTGSDLSN-- 133
 QY 273 AHFDLQMPGGGVIYNGCATOWGAPTDGARGVSSASDCSNLPSALQAGCKMRFGWF 332
 Db 134 -QFDLAIPEGGVIGYNGCTAQSGAPADGMSRGVSSRSRSCQSLPSGLQAGCQMRFDWF 192
 QY 333 KNADNPTMYKYVTCPEKAITAKSGCSR 359
 Db 193 QNADNPSINFNVQTCPELTAIKNCR 219

RESULT 4

Q9JH83 PRELIMINARY; PRT; 220 AA.
 AC Q9JH83; 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 OX NCBI_TaxID=42452;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
 RT "Diverse genes of family 45 cellulase homologues of the symbiotic
 RT protists in the hindgut of termite Reticulitermes speratus.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB045167; BAA98037.1; -
 DR EMBL: AB045166; BAA98036.1; -
 DR HSSP: P43316; 2ENG.
 DR InterPro: IPR000334; GH_45.
 DR Pfam: PF02015; Glyco_hydro_45; 1.
 DR PROSITE: PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
 SQ SEQUENCE 220 AA; 23108 MW; 97738D831BCFA5F3 CRC64;

Query Match 37.5%; Score 734; DB 14; Length 220;
 Best Local Similarity 63.8%; Pred. No. 1.1e-38;
 Matches 132; Conservative 23; Mismatches 46; Indels 6; Gaps 4;

QY 155 NGETTRYWDCCKPSCSWPGKADVTSPVSGCNKDGT-LADNNT-QNGCVGSSITCNDQ 212
 Db 17 SGKTRTRYWDCCKSGCMEKKADVSKPIIDTCADGTRVASNDTVSGCDGDDGYMCYDQ 76
 QY 213 PMVVSDDLAVGFAAASISGSEATWCCACFELFTSTAVKGMVQVNTGSDLSNTG 272
 Db 77 PMVNDSTVALGFPAASISGSEATWCCACFELFTSGPVGKMMVQVNTGSDLSN-- 133
 QY 273 AHFDLQMPGGGVIYNGCATOWGAPTDGARGVSSASDCSNLPSALQAGCKMRFGWF 332
 Db 134 -QFDLAIPEGGVIGYNGCTAQSGAPADGMSRGVSSRSRSCQSLPSGLQAGCQMRFDWF 192
 QY 333 KNADNPTMYKYVTCPEKAITAKSGCSR 359
 Db 193 QNADNPSINFNVQTCPELTAIKNCR 219

RESULT 5

Q9JH91 PRELIMINARY; PRT; 219 AA.
 AC Q9JH91;

RT protists in the hindgut of termite Reticulitermes speratus.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045175; BAA98045.1; -
DR HSSP; P43316; ZENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
SQ SEQUENCE 219 AA; 23030 MW; 179BF1344C6D7024 CRC64;

Query Match 37.2%; Score 727; DB 14; Length 219;
Best Local Similarity 62.8%; Pred. No. 3e-38;
Matches 130; Conservative 25; Mismatches 46; Indels 6; Gaps 4;

OY 155 NGETTRVWDCCPSGMPGKADVTSPVGSCKNDGKT-LADNNT-QNGCVGSSSYTCNDNQ 212
DB 16 SGTTRVWDCCCKSGCMERKANVDKPIDTCADGTRVASNDIVKSGCDGDDGFWCYDQT 75
OY 213 PMVVSDDLAVGFPAASISGSEATWCCACPELFTSTAVKGMVYVNTGSDLSGNTG 272
DB 76 PMQVSDSLSTGFPAALACCGG-ESGACCCGCTELFTTSGPVNKKMTVQITNTGGDLGSN-- 132
OY 273 AHFDLQMPGGGVGIVNGCATQWGAPTDGMGARVGVSSASDCSNLPSALQAGCKMRFGWF 332
DB 133 -QFDLAIPEGGVGIVNGCTSQSGAPADGWSRGVSSRSBSCQLPSGLQAGCMRFDWF 191
OY 333 KNADNPMTYKQVTCPEKAITAKSGCSR 359
DB 192 ANADNPINFTVVKCPSELIAKTNCNR 218

RESULT 9

O9JH89 PRELIMINARY; PRT; 219 AA.
ID O9JH89
AC O9JH89; 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DR 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RL protists in the hindgut of termite Reticulitermes speratus.";
Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045174; BAA98044.1; -
DR HSSP; P43316; ZENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
SQ SEQUENCE 219 AA; 23033 MW; CA295CAD8F393199 CRC64;

Query Match 37.0%; Score 724; DB 14; Length 219;
Best Local Similarity 62.3%; Pred. No. 4.6e-38;
Matches 129; Conservative 27; Mismatches 45; Indels 6; Gaps 4;

OY 155 NGETTRVWDCCPSGMPGKADVTSPVGSCKNDGKT-LADNNT-QNGCVGSSSYTCNDNQ 212
DB 16 SGTTRVWDCCCKSGCMERKANVDKPIDTCADGTRVASNDIVKSGCDGDDGFWCYDQT 75
OY 213 PMVVSDDLAVGFPAASISGSEATWCCACPELFTSTAVKGMVYVNTGSDLSGNTG 272
DB 76 PMQVSDSLSTGFPAALACCGG-ESGACCCGCTELFTTSGPVNKKMTVQITNTGGDLGSN-- 132
OY 273 AHFDLQMPGGGVGIVNGCATQWGAPTDGMGARVGVSSASDCSNLPSALQAGCKMRFGWF 332
DB 133 -QFDLAIPEGGVGIVNGCTSQSGAPADGWSRGVSSRSBSCQLPSGLQAGCMRFDWF 191
OY 333 KNADNPMTYKQVTCPEKAITAKSGCSR 359
DB 192 ANADNPINFTVVKCPSELIAKTNCNR 218

RESULT 10

O9JH94 PRELIMINARY; PRT; 221 AA.
ID O9JH94
AC O9JH94; 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DR 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RL protists in the hindgut of termite Reticulitermes speratus.";
Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045169; BAA98039.1; -
DR HSSP; P43316; ZENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
SQ SEQUENCE 221 AA; 23220 MW; BA84CEB0A8C6372 CRC64;

Query Match 36.9%; Score 721; DB 14; Length 221;
Best Local Similarity 60.9%; Pred. No. 7.2e-38;
Matches 126; Conservative 29; Mismatches 46; Indels 6; Gaps 4;

OY 155 NGETTRVWDCCPSGMPGKADVTSPVGSCKNDGKT-LADNNT-QNGCVGSSSYTCNDNQ 212
DB 17 SGTTRVWDCCCKSGCMERKANVDKPIDTCADGTRVASNDIVKSGCDGDDGFWCYDQT 76
OY 213 PMVVSDDLAVGFPAASISGSEATWCCACPELFTSTAVKGMVYVNTGSDLSGNTG 272
DB 77 PMAVNDSTSLGFPAALAVSGGKKA-CCQCYELFTTSGPVNKKMTVQITNTGGDLGSN-- 133
OY 273 AHFDLQMPGGGVGIVNGCATQWGAPTDGMGARVGVSSASDCSNLPSALQAGCKMRFGWF 332
DB 134 -QFDLAIPEGGVGIVNGCTSQSGAPADGWSRGVSSRSBSCQLPSGLQAGCMRFDWF 192
OY 333 KNADNPMTYKQVTCPEKAITAKSGCSR 359
DB 193 QNADNPINFTVVKCPSELIAKTNCNR 219

RESULT 11

O9JH93 PRELIMINARY; PRT; 220 AA.
ID O9JH93
AC O9JH93; 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DR 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RL protists in the hindgut of termite Reticulitermes speratus.";
Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045170; BAA98040.1; -
DR HSSP; P43316; ZENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
SQ SEQUENCE 220 AA; 23091 MW; 35F174F9B79C2D65 CRC64;

Query Match 36.6%; Score 715; DB 14; Length 220;
Best Local Similarity 62.1%; Pred. No. 1.7e-37;

Matches	128;	Conservative	23;	Mismatches	49;	Indels	6;	Gaps	4;
Qy	156	GETTRRYWDCCPCPSGSPGKADVTSPVSGCNQDKT-LADNNT-ONGCYGASSYTCNDNOP	213						
Db	18	GRTRRYMDCCCGSGCGMEKKANVDKEDIDCAKDGTTRVASNIVVSGCGDGGDGYMCYDOSP	77						
Qy	214	WVSPDDLAAYGPAALASISGSGSEATWCCACFELFTSTAVKGMVQVNTGSDLSNTGA	273						
Db	78	WGVNDSFALGPAALAVSGGSESHA-CNCCEYELFTSTGPNVNGKMTVQVNTGSDLSN---	133						
Qy	274	HFDLQMPGGGVGYINGCATOWCAPTDGNGARYGVVSSASDCSNLPSALOAGCKMFGWFK	333						
Db	134	QFDLAIPEGGVGYINGCATOWGAPADMGNGSRICGVVSSSECCQLPSGLQAGQWRFDWFO	193						
Qy	334	NADNPTMTYKQVTCPKAITAKSGCR 359							
Db	194	NADNPSIFNVVSCPSLEIAKTCRR 219							
RESULT 12									
ID	Q9JH85	PRELIMINARY;	PRT;	218	AA.				
AC	Q9JH85								
DT	01-OCT-2000	(TREMBLrel. 15, Created)							
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)							
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)							
DE	Family 45 cellulase homologue.								
OS	unclassified eukaryotes.								
OC	Eukaryota.								
OX	NCBI_TaxID=42452;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RA	Ohoko K., Ohkuma M., Moriya S., Kudo T.;								
RT	"Diverse genes of family 45 cellulase homologues of the symbiotic								
RL	protists in the hindgut of termite Reticulitermes speratus."								
RL	Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.								
DR	EMBL; AB045178; BAA98048.1; ..								
DR	HSSP; P43316; 3ENG.								
DR	InterPro; IPR000334; GH_45.								
DR	Pfam; PF02015; GLYCOSYL_HYDROL_F45; UNKOWN 1.								
DR	PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKOWN 1.								
SEQ	SEQUENCE 218 AA; 22680 MW; A600FF5B990AD43 CRC64;								
Query Match 36.5%; Score 714.5; DB 14; Length 218;									
Best Local Similarity 60.4%; Pred. No. 1.8e-37;									
Matches 125; Conservative 30; Mismatches 47; Indels 5; Gaps 3;									
Qy	155	NGETTRRYWDCCPCPSGSPGKADVTSPVSGCNQDKT-LADNNTQNGC-VGGSSYTCNDNOP	213						
Db	16	DGRTRRYWDCCCGSGCGMKASVSRKVPDTCADGTRTRAATSAKASDCSGTAYMCYDQTP	75						
Qy	214	WVSPDDLAAYGPAALASISGSGSEATWCCACFELFTSTAVVKGMMVQVNTGSDLSNTGA	273						
Db	76	RAVNDSTAIIGPAAALVSGGSEKKA-CCTCYELFTSTGPNVNGKMTVQVNTGSDLSN---	131						
Qy	274	HFDLQMPGGGVGYINGCATOWCAPTDGNGARYGVVSSASDCSNLPSALOAGCKMFGWFK	333						
Db	132	QFDLAIPEGGVGYINGCATOWGAPADMGNGSRICGVVSSSECCQLPSGLQAGQWRFDWFO	191						
Qy	334	NADNPTMTYKQVTCPKAITAKSGCR 360							
Db	192	NADNPSIFNVVSCPDILTSKTCRRQ 218							
RESULT 13									
ID	Q9JH96	PRELIMINARY;	PRT;	220	AA.				
AC	Q9JH96;								
DT	01-OCT-2000	(TREMBLrel. 15, Created)							
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)							
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)							
DE	Family 45 cellulase homologue.								
OS	unclassified eukaryotes.								

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OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RL proteases in the hindgut of termite Reticulitermes speratus";
DR EMBL; AB045167; BAA98035.1; -.
DR HSSP; P43316; ZENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
SQ SEQUENCE 220 AA; 23148 MW; 4F0652FB8BD269D5 CRC64;

Query Match          36.4%; Score 712; DB 14; Length 220;
Best Local Similarity 62.3%; Pred. No. 2,6e-37;
Matches 129; Conservative 23; Mismatches 49; Indels 6; Gaps 4

QY NGERTTRWDDCKRPGSCWPGRKADVTSPVSCMKDKGT-LADNNT--ONGCVGSSSYTCNDNQ 212
DB SGRTTTRYWDCCKGSGCGEMAKADVSKPIDTKCKDGTTRVASNDTVASGCDGBGYNCYDT 76
QY PMVVSDDLAYGFPAASISGSSEATWCACAFELTFSTVAVKKKMNVQYTNGSDIGSNTG 272
DB PRAYVDSYAIFPALAASISGEKA--CCCYELLFTFSGVNGKMTVQYTNGSDIGSN-- 133
QY AHFDLOMPGGVGIVNGCATOMGAPTDMGARVYGVSASSDCSNLPALQAGCKMRFGWF 332
DB -QFDLAIRGGVGIVNGCTAQASGAPADMGSRVYGVSSRSQCQLPSGLQGCGQRFDWMF 192
QY 333 KNADNPWTYVQTVCPRKAITKGCSCR 359
DB :::: :::::

Db 193 QNADNP SINFNVS CPELIANTNCR 219

RESULT 14
QJUH86 PRELIMINARY; PRT; 219 AA.
AC QJUH86;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
CX NCBI_TaxID=42452;
RX [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RL proteases in the hindgut of termite Reticulitermes speratus.";
DR EMBL; AB045177; BAA98047.1; -.
DR HSSP; P43316; ZENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
SQ SEQUENCE 219 AA; 23158 MW; ECD68EEABED1DI CRC64;

Query Match          36.3%; Score 711; DB 14; Length 219;
Best Local Similarity 60.9%; Pred. No. 3e-37;
Matches 126; Conservative 27; Mismatches 48; Indels 6; Gaps 4

QY NGETTRRYDDCKRPGSCWPGRKADVTSPVSCMKDKGT-LADNNT--ONGCVGSSSYTCNDNQ 212
DB SGKTTTRYWDCCKGSGCGEKKANVDPIPTCAXDGTTTRVASNITVASGCCDGGEGMYNCYDT 75
QY PMVVSDDLAYGFPAASISGSSEATWCACAFELTFSTVAVKKKMNVQYTNGSDIGSNTG 272
DB PRSVVDSYSYGPAAAACCAG--ESAGCCCCTDITFTFSGVNGKMIVQLTINCGDLSGN-- 132
QY 273 AHFDLOMPGGVGIVNGCATOMGAPTDMGARVYGVSASSDCSNLPALQAGCKMRFGWF 332
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